



PCT

RAW SEQUENCE LISTING

DATE: 10/24/2005

PATENT APPLICATION: US/10/552,786

TIME: 10:49:40

Input Set : A:\SEQLIST.txt

Output Set: N:\CRF4\10242005\J552786.raw

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5 <110> APPLICANT: DEPERTHES, David
6   CLOUTIER, Sylvain
9 <120> TITLE OF INVENTION: Inhibitor proteins of a protease and use thereof
12 <130> FILE REFERENCE: KZI-003US
C--> 15 <140> CURRENT APPLICATION NUMBER: US/10/552,786
C--> 15 <141> CURRENT FILING DATE: 2005-10-03
15 <150> PRIOR APPLICATION NUMBER: PCT/IB2004/001040
16 <151> PRIOR FILING DATE: 2004-04-05
19 <150> PRIOR APPLICATION NUMBER: US 60/460345
20 <151> PRIOR FILING DATE: 2003-04-04
24 <160> NUMBER OF SEQ ID NOS: 22
28 <170> SOFTWARE: PatentIn version 3.1
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34 <211> LENGTH: 1239
36 <212> TYPE: DNA
38 <213> ORGANISM: Artificial sequence
42 <220> FEATURE:
44 <223> OTHER INFORMATION: DNA Sequence ACT variants : MD 820
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51 gccaacgtgg acttcgcttt cagcctgtac aagcagttag tcctgaaggc ccctgataag      180
53 aatgtcatct tctccccact gagcatctcc accgccttgg ccttcctgtc tctggggggcc      240
55 cataatacca ccctgacaga gattctcaaa ggctcaagt tcaacctcac ggagacttct      300
57 gaggcagaaa ttcaccagag cttccagcac ctccctgcga ccctcaatca gtccagcgat      360
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61 aggttcacgg aggatgccaa gaggtgtat ggctccgagg cctttgccac tgactttcag      480
63 gactcagctg cagctaagaa gctcatcaac gactacgtga agaatggaac tagggggaaa      540
65 atcacagatc tgatcaagga ccttgactcg cagacaatga tggctcctgg gaattacatc      600
67 ttcttttaaag ccaaattggga gatgcccttt gacccccaa atactcatca gtcaagggttc      660
69 tacttgagca agaaaaagtg ggtaatggtg cccatgatga gtttgcatca cctgactata      720
71 ccttacttcc gggacgagga gctgtcctgc accgtggtgg agctgaagta cacaggcaat      780
73 gccagcgcac tcttcatact ccctgatcaa gacaagatgg aggaagtgga agccatgctg      840
75 ctcccagaga ccctgaagcg gtggagagac tctctggagt tcagagagat aggtgagctc      900
77 tacctgccaa agttttccat ctcgagggac tataacctga acgacatact tctccagctg      960
79 ggcattgagg aagccttcac cagcaaggct gacctgtcag ggatcacagg ggccagggaac     1020
81 ctagcagctc cccagggtgg ccataaggct gtgcttgatg tatttgagga gggcacagaa     1080
83 gcatctgctg ccaccgcggt caaaatcacc ctccgttctc gagcagtgga gacgcgtacc     1140
85 attgtgcggt tcaacaggcc ctctctgatg atcattgtcc ctacagacac ccagaacatc     1200
87 ttcttcatga gcaaagtcac caatcccaag caagcctaa      1239
90 <210> SEQ ID NO: 2
92 <211> LENGTH: 412
94 <212> TYPE: PRT

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96 <213> ORGANISM: Artificial sequence

100 <220> FEATURE:

102 <223> OTHER INFORMATION: Protein Sequence ACT variants : MD 820

104 <400> SEQUENCE: 2

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110 Pro Leu Asp Glu Glu Asn Leu Thr Gln Glu Asn Gln Asp Arg Gly Thr
111          20          25          30
114 His Val Asp Leu Gly Leu Ala Ser Ala Asn Val Asp Phe Ala Phe Ser
115          35          40          45
118 Leu Tyr Lys Gln Leu Val Leu Lys Ala Pro Asp Lys Asn Val Ile Phe
119          50          55          60
122 Ser Pro Leu Ser Ile Ser Thr Ala Leu Ala Phe Leu Ser Leu Gly Ala
123 65          70          75          80
126 His Asn Thr Thr Leu Thr Glu Ile Leu Lys Gly Leu Lys Phe Asn Leu
127          85          90          95
130 Thr Glu Thr Ser Glu Ala Glu Ile His Gln Ser Phe Gln His Leu Leu
131          100         105         110
134 Arg Thr Leu Asn Gln Ser Ser Asp Glu Leu Gln Leu Ser Met Gly Asn
135          115         120         125
138 Ala Met Phe Val Lys Glu Gln Leu Ser Leu Leu Asp Arg Phe Thr Glu
139          130         135         140
142 Asp Ala Lys Arg Leu Tyr Gly Ser Glu Ala Phe Ala Thr Asp Phe Gln
143 145          150         155         160
146 Asp Ser Ala Ala Ala Lys Lys Leu Ile Asn Asp Tyr Val Lys Asn Gly
147          165         170         175
150 Thr Arg Gly Lys Ile Thr Asp Leu Ile Lys Asp Leu Asp Ser Gln Thr
151          180         185         190
154 Met Met Val Leu Val Asn Tyr Ile Phe Phe Lys Ala Lys Trp Glu Met
155          195         200         205
158 Pro Phe Asp Pro Gln Asp Thr His Gln Ser Arg Phe Tyr Leu Ser Lys
159          210         215         220
162 Lys Lys Trp Val Met Val Pro Met Met Ser Leu His His Leu Thr Ile
163 225          230         235         240
166 Pro Tyr Phe Arg Asp Glu Glu Leu Ser Cys Thr Val Val Glu Leu Lys
167          245         250         255
170 Tyr Thr Gly Asn Ala Ser Ala Leu Phe Ile Leu Pro Asp Gln Asp Lys
171          260         265         270
174 Met Glu Glu Val Glu Ala Met Leu Leu Pro Glu Thr Leu Lys Arg Trp
175          275         280         285
178 Arg Asp Ser Leu Glu Phe Arg Glu Ile Gly Glu Leu Tyr Leu Pro Lys
179          290         295         300
182 Phe Ser Ile Ser Arg Asp Tyr Asn Leu Asn Asp Ile Leu Leu Gln Leu
183 305          310         315         320
186 Gly Ile Glu Glu Ala Phe Thr Ser Lys Ala Asp Leu Ser Gly Ile Thr
187          325         330         335
190 Gly Ala Arg Asn Leu Ala Val Ser Gln Val Val His Lys Ala Val Leu
191          340         345         350
194 Asp Val Phe Glu Glu Gly Thr Glu Ala Ser Ala Ala Thr Ala Val Lys

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195          355          360          365
198 Ile Thr Leu Arg Ser Arg Ala Val Glu Thr Arg Thr Ile Val Arg Phe
199          370          375          380
202 Asn Arg Pro Phe Leu Met Ile Ile Val Pro Thr Asp Thr Gln Asn Ile
203 385          390          395          400
206 Phe Phe Met Ser Lys Val Thr Asn Pro Lys Gln Ala
207          405          410
210 <210> SEQ ID NO: 3
212 <211> LENGTH: 1239
214 <212> TYPE: DNA
216 <213> ORGANISM: Artificial sequence
220 <220> FEATURE:
222 <223> OTHER INFORMATION: DNA Sequence ACT variant : MD 62
224 <400> SEQUENCE: 3
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229 gccaacgtgg acttcgcttt cagcctgtac aagcagttag tctgaaggc ccctgataag      180
231 aatgtcatct tctcccact gagcatctcc accgccttgg ccttctgtc tctgggggccc      240
233 cataatacca ccctgacaga gattctcaaa ggcctcaagt tcaacctcac ggagacttct      300
235 gaggcagaaa ttcaccagag cttccagcac ctctgcgca ccctcaatca gtccagcgat      360
237 gagctgcagc tgagtatggg aaatgccatg tttgtcaaag agcaactcag tctgctggac      420
239 aggttcacgg aggatgccaa gaggtgttat ggctccgagg cctttgccac tgactttcag      480
241 gactcagctg cagctaagaa gctcatcaac gactacgtga agaatggaac tagggggaaa      540
243 atcacagatc tgatcaagga ccttgactcg cagacaatga tggctctggg gaattacatc      600
245 ttctttaaag ccaaattggga gatgcccttt gacccccaa atactcatca gtcaagggttc      660
247 tacttgagca agaaaaagtg ggtaatggtg cccatgatga gtttgcacat cctgactata      720
249 ccttacttcc gggacgagga gctgtcctgc accgtggtgg agctgaagta cacaggcaat      780
251 gccagcgcac tcttcaccc cctgatcaa gacaagatgg aggaagtgga agccatgctg      840
253 ctcccagaga ccctgaagcg gtggagagac tctctggagt tcagagagat aggtgagctc      900
255 tacctgccaa agttttccat ctcgagggac tataacctga acgacatact tctccagctg      960
257 ggcattgagg aagccttcac cagcaaggct gacctgtcag ggatcacagg ggccaggaac     1020
259 ctagcagtct ccagggtggt ccataaggct gtgcttgatg tatttgagga gggcacagaa     1080
261 gcatctgctg ccaccgcggt caaatcacc aggaggtcta tcgatgtgga gacgcgtacc     1140
263 attgtgcgtt tcaacaggcc cttcctgatg atcattgtcc ctacagacac ccagaacatc     1200
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272 <212> TYPE: PRT
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278 <220> FEATURE:
280 <223> OTHER INFORMATION: Protein Sequence ACT variant : MD 62
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288 Pro Leu Asp Glu Glu Asn Leu Thr Gln Glu Asn Gln Asp Arg Gly Thr
289          20          25          30
292 His Val Asp Leu Gly Leu Ala Ser Ala Asn Val Asp Phe Ala Phe Ser
293          35          40          45
296 Leu Tyr Lys Gln Leu Val Leu Lys Ala Pro Asp Lys Asn Val Ile Phe

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297      50              55              60
300 Ser Pro Leu Ser Ile Ser Thr Ala Leu Ala Phe Leu Ser Leu Gly Ala
301 65              70              75              80
304 His Asn Thr Thr Leu Thr Glu Ile Leu Lys Gly Leu Lys Phe Asn Leu
305              85              90              95
308 Thr Glu Thr Ser Glu Ala Glu Ile His Gln Ser Phe Gln His Leu Leu
309              100              105              110
312 Arg Thr Leu Asn Gln Ser Ser Asp Glu Leu Gln Leu Ser Met Gly Asn
313              115              120              125
316 Ala Met Phe Val Lys Glu Gln Leu Ser Leu Leu Asp Arg Phe Thr Glu
317              130              135              140
320 Asp Ala Lys Arg Leu Tyr Gly Ser Glu Ala Phe Ala Thr Asp Phe Gln
321 145              150              155              160
324 Asp Ser Ala Ala Ala Lys Lys Leu Ile Asn Asp Tyr Val Lys Asn Gly
325              165              170              175
328 Thr Arg Gly Lys Ile Thr Asp Leu Ile Lys Asp Leu Asp Ser Gln Thr
329              180              185              190
332 Met Met Val Leu Val Asn Tyr Ile Phe Phe Lys Ala Lys Trp Glu Met
333              195              200              205
336 Pro Phe Asp Pro Gln Asp Thr His Gln Ser Arg Phe Tyr Leu Ser Lys
337              210              215              220
340 Lys Lys Trp Val Met Val Pro Met Met Ser Leu His His Leu Thr Ile
341 225              230              235              240
344 Pro Tyr Phe Arg Asp Glu Glu Leu Ser Cys Thr Val Val Glu Leu Lys
345              245              250              255
348 Tyr Thr Gly Asn Ala Ser Ala Leu Phe Ile Leu Pro Asp Gln Asp Lys
349              260              265              270
352 Met Glu Glu Val Glu Ala Met Leu Leu Pro Glu Thr Leu Lys Arg Trp
353              275              280              285
356 Arg Asp Ser Leu Glu Phe Arg Glu Ile Gly Glu Leu Tyr Leu Pro Lys
357              290              295              300
360 Phe Ser Ile Ser Arg Asp Tyr Asn Leu Asn Asp Ile Leu Leu Gln Leu
361 305              310              315              320
364 Gly Ile Glu Glu Ala Phe Thr Ser Lys Ala Asp Leu Ser Gly Ile Thr
365              325              330              335
368 Gly Ala Arg Asn Leu Ala Val Ser Gln Val Val His Lys Ala Val Leu
369              340              345              350
372 Asp Val Phe Glu Glu Gly Thr Glu Ala Ser Ala Ala Thr Ala Val Lys
373              355              360              365
376 Ile Thr Arg Arg Ser Ile Asp Val Glu Thr Arg Thr Ile Val Arg Phe
377              370              375              380
380 Asn Arg Pro Phe Leu Met Ile Ile Val Pro Thr Asp Thr Gln Asn Ile
381 385              390              395              400
384 Phe Phe Met Ser Lys Val Thr Asn Pro Lys Gln Ala
385              405              410
388 <210> SEQ ID NO: 5
390 <211> LENGTH: 1239
392 <212> TYPE: DNA
394 <213> ORGANISM: Artificial sequence

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398 <220> FEATURE:

400 <223> OTHER INFORMATION: DNA Sequence ACT variant : MD 83

402 <400> SEQUENCE: 5

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407 gccaacgtgg acttcgcttt cagcctgtac aagcagttag tcctgaaggc ccctgataag      180
409 aatgtcatct tctccccact gagcatctcc accgccttgg ccttcctgtc tctgggggcc      240
411 cataatacca ccctgacaga gattctcaaa ggctcaagt tcaacctcac ggagacttct      300
413 gaggcagaaa ttcaccagag cttccagcac ctctgcgca ccctcaatca gtccagcgat      360
415 gagctgcagc tgagtatggg aaatgccatg tttgtcaaag agcaactcag tctgctggac      420
417 aggttcacgg aggatgccaa gaggtgtgat ggctccgagg cctttgccac tgactttcag      480
419 gactcagctg cagctaagaa gctcatcaac gactacgtga agaatggaac tagggggaaa      540
421 atcacagatc tgatcaagga ccttgactcg cagacaatga tggtcctggg gaattacatc      600
423 ttcttttaaag ccaaattggga gatgcccttt gacccccaaag atactcatca gtcaagggttc      660
425 tacttgagca agaaaaagtg ggtaatggtg cccatgatga gtttgcatca cctgactata      720
427 ccttacttcc gggacgagga gctgtcctgc accgtggtgg agctgaagta cacaggcaat      780
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431 ctcccagaga ccctgaagcg gtggagagac tctctggagt tcagagagat aggtgagctc      900
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437 ctagcagtcct cccagggtggg ccataaggct gtgcttgatg tatttgagga gggcacagaa     1080
439 gcatctgctg ccaccgcggt caaaatcagg gggagatctg agttagtgga gacgcgtacc     1140
441 attgtgcgtt tcaacaggcc cttcctgatg atcattgtcc ctacagacac ccagaacatc     1200
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458 <223> OTHER INFORMATION: Protein Sequence ACT variant : MD 83

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467 20          25          30
470 His Val Asp Leu Gly Leu Ala Ser Ala Asn Val Asp Phe Ala Phe Ser
471 35          40          45
474 Leu Tyr Lys Gln Leu Val Leu Lys Ala Pro Asp Lys Asn Val Ile Phe
475 50          55          60
478 Ser Pro Leu Ser Ile Ser Thr Ala Leu Ala Phe Leu Ser Leu Gly Ala
479 65          70          75          80
482 His Asn Thr Thr Leu Thr Glu Ile Leu Lys Gly Leu Lys Phe Asn Leu
483 85          90          95
486 Thr Glu Thr Ser Glu Ala Glu Ile His Gln Ser Phe Gln His Leu Leu
487 100         105         110
490 Arg Thr Leu Asn Gln Ser Ser Asp Glu Leu Gln Leu Ser Met Gly Asn
491 115         120         125
494 Ala Met Phe Val Lys Glu Gln Leu Ser Leu Leu Asp Arg Phe Thr Glu
495 130         135         140

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VERIFICATION SUMMARY

PATENT APPLICATION: US/10/552,786

DATE: 10/24/2005

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Output Set: N:\CRF4\10242005\J552786.raw

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L:15 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:1004 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:12,Line#:1000